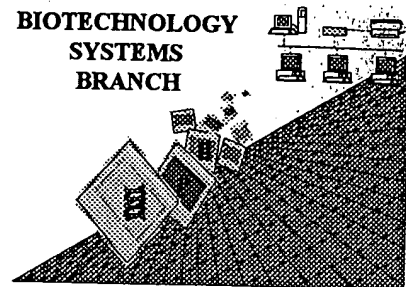


Draper



RAW SEQUENCE LISTING **ERROR REPORT**

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following CRF diskette:

Application Serial Number:

08/383,676

Art Unit / Team No. :

1646

Date Processed by STIC:

3/22/99

THE ATTACHED PRINTOUT EXPLAINS THE ERRORS DETECTED.

PLEASE BE SURE TO FORWARD THIS INFORMATION TO THE APPLICANTS BY EITHER:

- 1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANTS ALONG WITH A NOTICE TO COMPLY or,**
- 2) CALLING APPLICANTS AND FAXING THEM A COPY OF THE PRINTOUT WITH A NOTICE TO COMPLY**

THIS WILL INSURE THAT THE NEXT SUBMISSION RECEIVED FROM THEM WILL BE ERROR FREE.

IF YOU HAVE ANY FURTHER QUESTIONS, PLEASE CALL:

ARTI SHAH 703-308-4212

Raw Sequence Listing Error Summary

ERROR DETECTED SUGGESTED CORRECTION

SERIAL NUMBER:

08/383,676

ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE

- 1 Wrapped Nucleics The number/text at the end of each line "wrapped" down to the next line.
This may occur if your file was retrieved in a word processor after creating it.
Please adjust your right margin to .3, as this will prevent "wrapping".
- 2 Wrapped Aminos The amino acid number/text at the end of each line "wrapped " down to the next line.
This may occur if your file was retrieved in a word processor after creating it.
Please adjust your right margin to .3, as this will prevent "wrapping".
- 3 J Incorrect Line Length The rules require that a line not exceed 72 characters in length. This includes spaces.
All text must be visible on page.
- 4 Misaligned Amino Acid The numbering under each 5th amino acid is misaligned. This may be caused by the use of tabs
Numbering between the numbering. It is recommended to delete any tabs and uses spacing between the numbers.
- 5 Non-ASCII This file was not saved in ASCII (DOS) text, as required by the Sequence Rules.
Please ensure your subsequent submission is saved in ASCII text so that it can be processed.
- 6 Variable Length Sequence(s) contain n's or Xaa's which represented more than one residue.
As per the rules, each n or Xaa can only represent a single residue.
Please present the maximum number of each residue having variable length and
indicate in the (ix) features section that some may be missing.
- 7 Wrong Designation Sequence(s) contain amino acid or nucleic acid designators which are not standard
representations as per the Sequence Rules (Please refer to paragraph 1.822)
- 8 Skipped Sequences Sequence(s) missing. If intentional, please use the following format for each skipped sequence:
(OLD RULES) (2) INFORMATION FOR SEQ ID NO:X:
 (i) SEQUENCE CHARACTERISTICS:(Do not insert any headings under "SEQUENCE CHARACTERISTICS")
 (xi) SEQUENCE DESCRIPTION:SEQ ID NO:X:
 This sequence is intentionally skipped

Please also adjust the "(iii) NUMBER OF SEQUENCES:" response to include the skipped sequence(s).
- 9 Skipped Sequences Sequence(s) missing. If intentional, please use the following format for each skipped sequence.
(NEW RULES) <210> sequence id number
 <400> sequence id number
 000
- 10 Use of n's or Xaa's Use of n's and/or Xaa's have been detected in the Sequence Listing.
(NEW RULES) Use of <220> to <223> is MANDATORY if n's or Xaa's are present.
 In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents.
- 11 Use of <213>Organism Sequence(s) are missing this mandatory field or its response.
(NEW RULES)
- 12 Use of <220>Feature Sequence(s) are missing the <220>Feature and associated headings.
(NEW RULES) Use of <220> to <223> is MANDATORY if <213>ORGANISM is "Artificial" or "Unknown"
 Please explain source of genetic material in <220> to <223> section.
 (See "Federal Register," 6/01/98, Vol. 63, No. 104, pp. 29631-32)
 (Sec. 1.823 of new Sequence Rules)
- 13 PatentIn ver. 2.0 "bug" Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted
file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing).
Instead, please use "File Manager" or any other means to copy file to floppy disk.

RAW SEQUENCE LISTING
PATENT APPLICATION US/08/383,676

DATE: 03/22/1999
 TIME: 13:50:51

INPUT SET: S31123.raw

This Raw Listing contains the General
 Information Section and those Sequences
 containing ERRORS.

SEQUENCE LISTING

Does Not Comply
 Corrected Diskette Needed

1
 2
 3 (1) General Information:
 4
 5 (i) APPLICANT: Hauptman, et al.
 6
 7 (ii) TITLE OF INVENTION: TNF RECEPTORS, TNF BINDINGBINDING PROTEINS, AND DNAs CODIN
 8
 9 (iii) NUMBER OF SEQUENCES: 64 *72 shown (p.19)*
 10
 11 (iv) CORRESPONDENCE ADDRESS:
 12 (A) ADDRESSEE: John J. McDonnell
 13 (B) STREET: 300 S. Wacker Drive
 14 (C) CITY: Chicago
 15 (D) STATE: IL
 16 (E) COUNTRY: USA
 17 (F) ZIP: 60606
 18
 19 (v) COMPUTER READABLE FORM:
 20 (A) MEDIUM TYPE: Floppy disk
 21 (B) COMPUTER: IBM PC compatible
 22 (C) OPERATING SYSTEM: PC-DOS/MS-DOS
 23 (D) SOFTWARE: ASCII
 24
 25 (vi) CURRENT APPLICATION DATA: *383,676*
 26 (A) APPLICATION NUMBER: 08/484,312
 27 (B) FILING DATE: June 7, 1995
 28 (C) CLASSIFICATION:
 29
 30 (viii) ATTORNEY/AGENT INFORMATION:
 31 (A) NAME: John J. McDonnell
 32 (B) REGISTRATION NUMBER: 26,949
 33 (C) REFERENCE/DOCKET NUMBER: 98,385-A
 34
 35 (ix) TELECOMMUNICATION INFORMATION:
 36 (A) TELEPHONE: 312-913-0001
 37 (B) TELEFAX: 312-913-9808
 38

all item 3 on Err Summary sheet

*Suggestion:
 Consult sequence Rules for valid format*

ERRORED SEQUENCES FOLLOW:

39 (2) INFORMATION FOR SEQ ID NO:1:

RAW SEQUENCE LISTING PATENT APPLICATION US/08/383,676

DATE: 03/22/1999
TIME: 13:50:52

INPUT SET: S31123.raw

40
--> 41 (i) SEQUENCE CHARACTERISTICS: *all text must be visible*
42 (A) LENGTH:1365 bases
43 (B) TYPE:nucleic acid
44 (C) STRANDEDNESS:single
45 (D) TOPOLOGY:linear
46
47 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:
48
49 ATGGGCCTCT CCACCGTGCC TGACCTGCTG CTGCCACTGG TGCTCCTGGA 50 GCTGTTGGTG GGAATATACC
50

insert hard returns after each cumulative base total

51 (2) INFORMATION FOR SEQ ID NO:2:
52
--> 53 (i) SEQUENCE CHARACTERISTICS:
54 (A) LENGTH:483 bases
55 (B) TYPE:nucleic acid
56 (C) STRANDEDNESS:single
57 (D) TOPOLOGY:linear
58
59 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:
60
61 GATAGTGTGT GTCCCAAGG AAAATATATC CACCCTCAAA ATAATTGAT 50 TTGCTGTACC AAGTGCCACA A
62

same error

63 (2) INFORMATION FOR SEQ ID NO:3:
64
--> 65 (i) SEQUENCE CHARACTERISTICS:
--> 66 (A) LENGTH:455 amino acids
--> 67 (B) TYPE:polypeptide *the only valid response is "amino acid"*
68 (D) TOPOLOGY: *add the mandatory subheading and response for all sequence types. This is a global error in the amino acid sequence.*
--> 69 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:
70
71 Met Gly Leu Ser Thr Val Pro Asp Leu Leu Leu Pro Leu Val Leu
72 5 10 15
73 Leu Glu Leu Leu Val Gly Ile Tyr Pro Ser Gly Val Ile Gly Leu
74 20 25 30
75 Val Pro His Leu Gly Asp Arg Glu Lys Arg Asp Ser Val Cys Pro
76 35 40 45
77 Gln Gly Lys Tyr Ile His Pro Gln Asn Asn Ser Ile Cys Cys Thr
78 50 55 60
79 Lys Cys His Lys Gly Thr Tyr Leu Tyr Asn Asp Cys Pro Gly Pro
80 65 70 75
81 Gly Gln Asp Thr Asp Cys Arg Glu Cys Glu Ser Gly Ser Phe Thr
82 80 85 90
83 Ala Ser Glu Asn His Leu Arg His Cys Leu Ser Cys Ser Lys Cys
84 95 100 105
85 Arg Lys Glu Met Gly Gln Val Glu Ile Ser Ser Cys Thr Val Asp
86 110 115 120
87 Arg Asp Thr Val Cys Gly Cys Arg Lys Asn Gln Tyr Arg His Tyr
88 125 130 135
89 Trp Ser Glu Asn Leu Phe Gln Cys Phe Asn Cys Ser Leu Cys Leu
90 140 145 150

RAW SEQUENCE LISTING PATENT APPLICATION US/08/383,676

DATE: 03/22/1999

TIME: 13:50:52

INPUT SET: S31123.raw

```

91  Asn Gly Thr Val His Leu Ser Cys Gln Glu Lys Gln Asn Thr Val
92                                155                                160                                165
93  Cys Thr Cys His Ala Gly Phe Phe Leu Arg Glu Asn Glu Cys Val
94                                170                                175                                180
95  Ser Cys Ser Asn Cys Lys Lys Ser Leu Glu Cys Thr Lys Leu Cys
96                                185                                190                                195
97  Leu Pro Gln Ile Glu Asn Val Lys Gly Thr Glu Asp Ser Gly Thr
98                                200                                205                                210
99  Thr Val Leu Leu Pro Leu Val Ile Phe Phe Gly Leu Cys Leu Leu
100                               215                               220                               225
101  Ser Leu Leu Phe Ile Gly Leu Met Tyr Arg Tyr Gln Arg Trp Lys
102                               230                               235                               240
103  Ser Lys Leu Tyr Ser Ile Val Cys Gly Lys Ser Thr Pro Glu Lys
104                               245                               250                               255
105  Glu Gly Glu Leu Glu Gly Thr Thr Thr Lys Pro Leu Ala Pro Asn
106                               260                               265                               270
107  Pro Ser Phe Ser Pro Thr Pro Gly Phe Thr Pro Thr Leu Gly Phe
108                               275                               280                               285
109  Ser Pro Val Pro Ser Ser Thr Phe Thr Ser Ser Ser Thr Tyr Thr
110                               290                               295                               300
111  Pro Gly Asp Cys Pro Asn Phe Ala Ala Pro Arg Arg Glu Val Ala
112                               305                               310                               315
113  Pro Pro Tyr Gln Gly Ala Asp Pro Ile Leu Ala Thr Ala Leu Ala
114                               320                               325                               330
115  Ser Asp Pro Ile Pro Asn Pro Leu Gln Lys Trp Glu Asp Ser Ala
116                               335                               340                               345
117  His Lys Pro Gln Ser Leu Asp Thr Asp Asp Pro Ala Thr Leu Tyr
118                               350                               355                               360
119  Ala Val Val Glu Asn Val Pro Pro Leu Arg Trp Lys Glu Phe Val
120                               365                               370                               375
121  Arg Arg Leu Gly Leu Ser Asp His Glu Ile Asp Arg Leu Glu Leu
122                               380                               385                               390
123  Gln Asn Gly Arg Cys Leu Arg Glu Ala Gln Tyr Ser Met Leu Ala
124                               395                               400                               405
125  Thr Trp Arg Arg Arg Thr Pro Arg Arg Glu Ala Thr Leu Glu Leu
126                               410                               415                               420
127  Leu Gly Arg Val Leu Arg Asp Met Asp Leu Leu Gly Cys Leu Glu
128                               425                               430                               435
129  Asp Ile Glu Glu Ala Leu Cys Gly Pro Ala Ala Leu Pro Pro Ala
130                               440                               445                               450
131  Pro Ser Leu Leu Arg
132                               455
133

```

134 (2) INFORMATION FOR SEQ ID NO:4:

135

136 (i) SEQUENCE CHARACTERISTICS:

--> 137 (A) LENGTH:161 amino acids

--> 138 (B) TYPE:polypeptide

139

--> 140 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

141

142 Asp Ser Val Cys Pro Gln Gly Lys Tyr Ile His Pro Gln Asn Asn

RAW SEQUENCE LISTING

PATENT APPLICATION US/08/383,676

DATE: 03/22/1999
TIME: 13:50:52

INPUT SET: S31123.raw

```

143          5          10          15
144 Ser Ile Cys Cys Thr Lys Cys His Lys Gly Thr Tyr Leu Tyr Asn
145          20          25          30
146 Asp Cys Pro Gly Pro Gly Gln Asp Thr Asp Cys Arg Glu Cys Glu
147          35          40          45
148 Ser Gly Ser Phe Thr Ala Ser Glu Asn His Leu Arg His Cys Leu
149          50          55          60
150 Ser Cys Ser Lys Cys Arg Lys Glu Met Gly Gln Val Glu Ile Ser
151          65          70          75
152 Ser Cys Thr Val Asp Arg Asp Thr Val Cys Gly Cys Arg Lys Asn
153          80          85          90
154 Gln Tyr Arg His Tyr Trp Ser Glu Asn Leu Phe Gln Cys Phe Asn
155          95          100         105
156 Cys Ser Leu Cys Leu Asn Gly Thr Val His Leu Ser Cys Gln Glu
157          110         115         120
158 Lys Gln Asn Thr Val Cys Thr Cys His Ala Gly Phe Phe Leu Arg
159          125         130         135
160 Glu Asn Glu Cys Val Ser Cys Ser Asn Cys Lys Lys Ser Leu Glu
161          140         145         150
162 Cys Thr Lys Leu Cys Leu Pro Gln Ile Glu Asn
163          155         160
164

```

165 (2) INFORMATION FOR SEQ ID NO:5:

166

167 (i) SEQUENCE CHARACTERISTICS:

--> 168 (A) LENGTH:157 bases

169 (B) TYPE:nucleic acid

170 (C) STRANDEDNESS:single

171 (D) TOPOLOGY:linear

172

173 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

174

175 CAGGGGAAA ATATTCACCC TCAAATAAT TCGATTTGCT GTACCAAGTG

176

50 CCACAAAGG AAACACTTGT TA

*hard returns**✓*

177 (2) INFORMATION FOR SEQ ID NO:6:

178

179 (i) SEQUENCE CHARACTERISTICS:

--> 180 (A) LENGTH:13 amino acids

--> 181 (B) TYPE:polypeptide

182

--> 183 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

184

185 Asp Ser Val Xaa Pro Gln Gly Lys Tyr Ile His Pro Gln

186

187

5

10

and add (D) TOPOLOGY: leading and response

188 (2) INFORMATION FOR SEQ ID NO:7:

189

190 (i) SEQUENCE CHARACTERISTICS:

--> 191 (A) LENGTH:11 amino acids

--> 192 (B) TYPE:polypeptide

same even

RAW SEQUENCE LISTING
PATENT APPLICATION US/08/383,676DATE: 03/22/1999
TIME: 13:50:53

INPUT SET: S31123.raw

193
--> 194 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:
195
196 Glu Asn Glu Cys Val Ser Cys Ser Asn Cys Lys
197 5 10
198

199 (2) INFORMATION FOR SEQ ID NO:8:
200
201 (i) SEQUENCE CHARACTERISTICS:
--> 202 (A) LENGTH:12 amino acids
--> 203 (B) TYPE:polypeptide
204
--> 205 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:
206
207 Glu Asn Glu Cys Val Ser Cys Ser Asn Cys Lys Lys
208 5 10
209

210 (2) INFORMATION FOR SEQ ID NO:9:
211
212 (i) SEQUENCE CHARACTERISTICS:
--> 213 (A) LENGTH:13 amino acids
--> 214 (B) TYPE:polypeptide
215
--> 216 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:
217
218 Tyr Ile His Pro Gln Xaa Asn Ser Ile Xaa Xaa Xaa Lys
219

220 (2) insert this number in all sequences - (2) remove
221 (11) INFORMATION FOR SEQ ID NO:10:
222
223 (i) SEQUENCE CHARACTERISTICS:
--> 224 (A) LENGTH:14 amino acids
--> 225 (B) TYPE:polypeptide
226
--> 227 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:
228
229 Glu Cys Glu Ser Gly Ser Phe Thr Ala Ser Glu Asn Asn Lys
230 5 10
231

--> 232 (2) INFORMATION FOR SEQ ID NO:11:
233
234 (i) SEQUENCE CHARACTERISTICS:
--> 235 (A) LENGTH:15 amino acids
--> 236 (B) TYPE:polypeptide
237
--> 238 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:
239
240 Lys Glu Met Gly Gln Val Glu Ile Ser Ser Cys Thr Val Asp Arg
241 5 10 15
242

RAW SEQUENCE LISTING
PATENT APPLICATION US/08/383,676DATE: 03/22/1999
TIME: 13:50:53

INPUT SET: S31123.raw

243 (2) INFORMATION FOR SEQ ID NO:12:
244
245 (i) SEQUENCE CHARACTERISTICS:
--> 246 (A) LENGTH:13 amino acids
--> 247 (B) TYPE:polypeptide
248
--> 249 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:
250
251 Gly Thr Tyr Ley Tyr Asn Asp Cys Pro Gly Pro Gly Gln
252 5 10
253

254 (2) INFORMATION FOR SEQ ID NO:13:
255
256 (i) SEQUENCE CHARACTERISTICS:
--> 257 (A) LENGTH:13 amino acids
--> 258 (B) TYPE:polypeptide
259
--> 260 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:
261
262 Glu Met Gly Gln Val Glu Ile Ser Xaa Xaa Xaa Val Asp
263 5 10
264

265 (2) INFORMATION FOR SEQ ID NO:14:
266
267 (i) SEQUENCE CHARACTERISTICS:
--> 268 (A) LENGTH:20 amino acids
--> 269 (B) TYPE:polypeptide
270
--> 271 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:
272
273 Lys Glu Met Gly Gln Val Glu Ile Ser Ser Cys Thr Val Asp Arg
274 5 10 15
275 Asp Thr Val Cys Gly
276 20
277

278 (2) INFORMATION FOR SEQ ID NO:15:
279
280 (i) SEQUENCE CHARACTERISTICS:
--> 281 (A) LENGTH:19 amino acids
--> 282 (B) TYPE:polypeptide
283
--> 284 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:
285
286 Tyr Ile His Pro Gln Xaa Asn Ser Ile Cys Cys Thr Lys Cys His
287 5 10 15
288 Lys Gly Xaa Tyr
289
290

291 (2) INFORMATION FOR SEQ ID NO:16:

RAW SEQUENCE LISTING
PATENT APPLICATION US/08/383,676DATE: 03/22/1999
TIME: 13:50:54

INPUT SET: S31123.raw

292
293 (i) SEQUENCE CHARACTERISTICS:
--> 294 (A) LENGTH:18 amino acids
--> 295 (B) TYPE:polypeptide
296
--> 297 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:
298
299 Gly Thr Tyr Leu Tyr Asn Asp Cys Pro Gly Pro Gly Gln Asp Thr
300 5 10 15
301 Xaa Xaa Arg
302
303

304 (2) INFORMATION FOR SEQ ID NO:17:
305
306 (i) SEQUENCE CHARACTERISTICS:
--> 307 (A) LENGTH:14 amino acids
--> 308 (B) TYPE:polypeptide
309
--> 310 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:17:
311
312 Gln Asn Thr Val Cys Thr Xaa His Ala Gly Phe Phe Leu Arg
313 5 10
314

315 (2) INFORMATION FOR SEQ ID NO:18:
316
317 (i) SEQUENCE CHARACTERISTICS:
--> 318 (A) LENGTH:14 amino acids
--> 319 (B) TYPE:polypeptide
320
--> 321 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:18:
322
323 Ser Leu Glu Cys Thr Lys Leu Cys Leu Pro Gln Ile Glu Asn
324 5 10
325

326 (2) INFORMATION FOR SEQ ID NO:19:
327
328 (i) SEQUENCE CHARACTERISTICS:
--> 329 (A) LENGTH:13 amino acids
--> 330 (B) TYPE:polypeptide
331
--> 332 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:19:
333
334 Asp Ser Val Cys Pro Gln Gly Lys Tyr Ile His Pro Gln
335 5 10
336

481 (2) INFORMATION FOR SEQ ID NO:32:
482
483 (i) SEQUENCE CHARACTERISTICS:
--> 484 (A) LENGTH:14 amino acids

RAW SEQUENCE LISTING
PATENT APPLICATION US/08/383,676

DATE: 03/22/1999

TIME: 13:50:54

INPUT SET: S31123.raw

--> 485 (B) TYPE: polypeptide
486
--> 487 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:32:
488
489 Glu Cys Gly Ser Gly Ser Phe Thr Ala Ser Glu Asn Asn Lys
490 5 10
491

492 (2) INFORMATION FOR SEQ ID NO:33:
493
494 (i) SEQUENCE CHARACTERISTICS:
--> 495 (A) LENGTH:14 amino acids
--> 496 (B) TYPE: polypeptide
497
--> 498 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:33:
499
500 Glu Cys Gly Ser Gly Ser Phe Thr Ala Ser Cys Asn Asn Lys
501 5 10
502

647 (2) INFORMATION FOR SEQ ID NO:46:
648
649 (i) SEQUENCE CHARACTERISTICS:
--> 650 (A) LENGTH:51 amino acids
--> 651 (B) TYPE: polypeptide
652
--> 653 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:46:
654
655 Gln Gly Lys Tyr Ile His Pro Gln Asn Asn Ser Ile Cys Cys Thr
656 5 10 15
657 Lys Cys His Lys Gly Thr Tyr Ley Tyr Asn Asp Cys Pro Gly Pro
658 20 25 30
659 Gly Gln Asp Thr Asp Cys Arg Gly Cys Glu Ser Gly Ser Phe Thr
660 35 40 45
661 Ala Ser Glu Asn Asn Lys
662 50
663

664 (2) INFORMATION FOR SEQ ID NO:47:
665
666 (i) SEQUENCE CHARACTERISTICS:
--> 667 (A) LENGTH:158 bases
668 (B) TYPE:nucleic acid
669 (C) STRANDEDNESS:single
670 (D) TOPOLOGY:linear
671
672 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:47:
673
674 CAGGGGAAAT ATATTCACCC TCAAATAAT TCGATTTCGT GTACCAAGTC 50 GCACAAAGGA ACCTACTTGT A
675

762 (2) INFORMATION FOR SEQ ID NO:55:
763

Hand return

RAW SEQUENCE LISTING
PATENT APPLICATION US/08/383,676DATE: 03/22/1999
TIME: 13:50:54

INPUT SET: S31123.raw

--> 764 (i) SEQUENCE CHARACTERISTICS:
765 (A) LENGTH:63 bases
766 (B) TYPE:nucleic acid
767 (C) STRANDEDNESS:single
768 (D) TOPOLOGY:linear
769
770 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:55:
771
772 AGCTCTAGAG ATTCGCGGCC GCTCGAGGTA CCGGATCCAT CGATGTCGAC 50 CTGCAGAAGC TTG
773

774 (2) INFORMATION FOR SEQ ID NO:56:
775
776 (i) SEQUENCE CHARACTERISTICS:
--> 777 (A) LENGTH:64 bases
778 (B) TYPE:nucleic acid
779 (C) STRANDEDNESS:single
780 (D) TOPOLOGY:linear
781
782 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:56:
783
784 CTAGCAAGCT TCTGCAGGTC GACATCGATG GATCCGGTAC CTCGAGCGGC 50 CGCGAATTCT CTAG
785

810 (2) INFORMATION FOR SEQ ID NO:59:
811
812 (i) SEQUENCE CHARACTERISTICS:
--> 813 (A) LENGTH:81 bases
814 (B) TYPE:nucleic acid
815 (C) STRANDEDNESS:single
816 (D) TOPOLOGY:linear
817
818 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:59:
819
820 CACAGTCGAC TTACATTTGC TTCTGACACA ACTGTGTTCA CTAGCAACCT 50 CAAACAGACA CCATGGGCCT C
821

870 (2) INFORMATION FOR SEQ ID NO:64:
871
872 (i) SEQUENCE CHARACTERISTICS:
--> 873 (A) LENGTH:30 bases 18 shown
874 (B) TYPE:nucleic acid
875 (C) STRANDEDNESS:single
876 (D) TOPOLOGY:linear
877
878 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:64:
879
880 GTCCAATTAT GTCACACC 18
881

882 (2) INFORMATION FOR SEQ ID NO:65:
883
884 (i) SEQUENCE CHARACTERISTICS:

RAW SEQUENCE LISTING PATENT APPLICATION US/08/383,676

 DATE: 03/22/1999
 TIME: 13:50:55

INPUT SET: S31123.raw

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--> 885 (A) LENGTH:1334 bases
      886 (B) TYPE:nucleic acid
      887 (C) STRANDEDNESS:single
      888 (D) TOPOLOGY:linear
      889
      890 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:65:
      891
      892 GAATTCTCTG GACTGAGGCT CCAGTTCTGG CCTTTGGGGT TCAAGATCAC 50 TGGGACCAGG CCGTGAT
      893
--> 894 TAGCTGTCTG GC 212
      895
      896 ATG GGC CTC TCC ACC GTG CCT GAC CTG CTG CTG CCA CTG GTG TTC 257
      897 Met Gly Leu Ser Thr Val Pro Asp Leu Leu Leu Pro Leu Val Leu
      898 5 10 15
      899
      900 CTG GAG CTG TTG GTG GGA ATA TAC CCC TCA GGG GTT ATT GGA CTG 302
      901 Leu Glu Leu Leu Val Gly Ile Tyr Pro Ser Gly Val Ile Gly Leu
      902 20 25 30
      903
      904 GTC CCT CAC CTA GGG GAC AGG GAG AAG AGA GAT AGT GTG TGT CCC 347
      905 Val Pro His Leu Gly Asp Arg Glu Lys Arg Asp Ser Val Cys Pro
      906 35 40 45
      907
      908 CAA GGA AAA TAT ATC CAC CCT CAA AAT AAT TCG ATT TGC TGT ACC 392
      909 Gln Gly Lys Tyr Ile His Pro Gln Asn Asn Ser Ile Cys Cys Thr
      910 50 55 60
      911
      912 AAG TGC CAC AAA GGA ACC TAC TTG TAC AAT GAC TGT CCA GGC CCG 437
      913 Lys Cys His Lys Gly Thr Tyr Leu Tyr Asn Asp Cys Pro Gly Pro
      914 65 70 75
      915
      916 GGG CAG GAT ACG GAC TGC AGG GAG TGT GAG AGC GGC TCC TTC ACC 482
      917 Gly Gln Asp The Asp Cys Arg Glu Cys Gly Ser Gly Ser Phe Thr
      918 80 85 90
      919
      920 GCT TCA GAA AAC CAC CTC AGA CAC TGC CTC AGC TGC TCC AAA TGC 527
      921 Ala Ser Glu Asn His Leu Arg His Cys Leu Ser Cys Ser Lys Cys
      922 95 100 105
      923
      924 CGA AAG GAA ATC GGT CAG GTG GAG ATC TCT TCT TGC ACA GTG GAC 572
      925 Arg Lys Glu Met Gly Gln Val Glu Ile Ser Ser Cys Thr Val Asp
      926 110 115 120
      927
      928 CGG GAC ACC GTG TGT GGC TGC AGG AAG AAC CAG TAC CGG CAT TAT 617
      929 Arg Asp Thr Val Cys Gly Cys Arg Lys Asn Gln Tyr Arg His Tyr
      930 125 130 135
      931
      932 TGG AGT GAA AAC CTTTTC CAG TGC TTC AAT TGC AGC CTC TGC CTC 662
      933 Trp Ser Glu Asn Leu Phe Gln Cys Phe Asn Cys Ser Leu Cys Leu
      934 140 145 150
      935
      936 AAT GGG ACC GTG CAC CTC TCC TGC CAG GAG AAA CAG AAC ACC GTG 707
      937 Asn Gly Thr Val His Leu Ser Cys Gln Glu Lys Gln Asn Thr Val
  
```

140L *procs are shown in submitted file - if this represents a gap in*
 150 *the sequence*
separate sequences
must be shown
(see 1.822(c) of
sequence rules for
annotation)

RAW SEQUENCE LISTING PATENT APPLICATION US/08/383,676

DATE: 03/22/1999
TIME: 13:50:55

INPUT SET: S31123.raw

	155	160	165	
938				
939				
940	TGC ACC TGC CAT GCA GGT TTC TTT CTA AGA GAA AAC GAG TGT GTC	752		
941	Cys Thr Cys His Ala Gly Phe Phe Leu Arg Glu Asn Glu Cys Val			
942	170	175	180	
943				
944	TCC TGT AGT AAC TGT AAG AAA AGC CTG GAG TGC AGG AAG TTG TGC	797		
945	Ser Cys Ser Asn Cys Lys Lys Ser Leu Glu Cys Thr Lys Leu Cys			
946	185	190	195	
947				
948	CTA CCC CAG ATT GAG AAT GTT AAG GGC ACT GAG GAC TCA GGC ACC	842		
949	Leu Pro Gln Ile Glu Asn Val Lys Gly Thr Glu Asp Ser Gly Thr			
950	200	205	210	
951				
952	ACA GTG CTG TTG CCC CTG GTC ATT TTC TTT GGT CTT TGC CTT TTA	887		
953	Thr Val Leu Leu ProLeu Val Ile Phe Phe Gly Leu Cys Leu Leu			
954	215	220	225	
955				
956	TCC CTC CTC TTC ATT GGT TTA ATG TAT CGC TAC CAA CGG TGG AAG	932		
957	Ser Leu Leu Phe Ile Gly Leu Met Tyr Arg Tyr Gln Arg Trp Lys			
958	230	235	240	
959				
960	TCC AAG CTC TAC TCC ATT GTT TGT GGG AAA TCG ACA CCT GAA AAA	977		
961	Ser Lys Leu Tyr Ser Ile Val Cys Gly Lys Ser Thr Pro Glu Lys			
962	245	250	255	
963				
964	GAG GGG GAG CTT GAA GGA ACT ACT ACT AAG CCC CTG GCC CCA AAC	1022		
965	Glu Gly Glu Leu Glu Gly Thr Thr Thr Lys Pro Leu Ala Pro Asn			
966	260	265	270	
967				
968	CCA AGC TTC AGT CCC ACT CCA GGC TTC ACC CCC ACC CTG GGC TTC	1067		
969	Pro Ser Phe Ser Pro Thr Pro Gly Phe Thr Pro Thr Leu Gly Phe			
970	275	280	285	
971				
972	AGT CCC GTG CCC AGT TCC ACC TTC ACC TCC AGC TCC ACC TAT ACC	1112		
973	Ser Pro Val Pro Ser Ser Thr Phe Thr Ser Ser Ser Thr Tyr Thr			
974	290	295	300	
975				
976	CCC GGT GAC TGT CCC AAC TTT GCG GCT CCC CGC AGA GAG GTG GCA	1157		
977	Pro Gly Asp Cys Pro Asn Phe Ala Ala Pro Arg Arg Glu Val Ala			
978	305	310	315	
979				
980	CCA CCC TAT CAG GGG GCT GAC CCC ATC CTT GCG ACA GCC CTC GCC	1202		
981	Pro Pro Tyr Gln Gly Ala Asp Pro Ile Leu Ala Thr Ala Leu Ala			
982	320	325	330	
983				
984	TCC GAC CCC ATC CCC AAC CCC CTT CAG AAG TGG GAG GAC AGC GCC	1247		
985	Ser Asp Pro Ile Pro Asn Pro Leu Gln Lys Trp Glu Asp Ser Ala			
986	335	340	345	
987				
988	CAC AAG CCA CAG AGC CTA GAC ACT GAT GAC CCC GCG ACG CTG TAC	1292		
989	His Lys Pro Gln Ser Leu Asp Thr Asp Asp Pro Ala Thr Leu Tyr			
990	350	355	360	

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991
992 GCC GTG GTG GAG AAC GTG CCC CCG TTG CGC TGG AAGGAATTC 1334
993 Ala Val Val Glu Asn Val Pro Pro Leu Arg Trp
994 365 370
995
996

997 (2) INFORMATION FOR SEQ ID NO:66:
998
999 (i) SEQUENCE CHARACTERISTICS:
--> 1000 (A) LENGTH: 371 amino acids
--> 1001 (B) TYPE: polypeptide
1002
--> 1003 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:66:
1004
1005 Met Gly Leu Ser Thr Val Pro Asp Leu Leu Leu Pro Leu Val Leu
1006 5 10 15
1007 Leu Glu Leu Leu Val Gly Ile Tyr Pro Ser Gly Val Ile Gly Leu
1008 20 25 30
1009 Val Pro His Leu Gly Asp Arg Glu Lys Arg Asp Ser Val Cys Pro
1010 35 40 45
1011 Gln Gly Lys Tyr Ile His Pro Gln Asn Asn Ser Ile Cys Cys Thr
1012 50 55 60
1013 Lys Cys His Lys Gly Thr Tyr Leu Tyr Asn Asp Cys Pro Gly Pro
1014 65 70 75
1015 Gly Gln Asp The Asp Cys Arg Glu Cys Gly Ser Gly Ser Phe Thr
1016 80 85 90
1017 Ala Ser Glu Asn His Leu Arg His Cys Leu Ser Cys Ser Lys Cys
1018 95 100 105
1019 Arg Lys Glu Met Gly Gln Val Glu Ile Ser Ser Cys Thr Val Asp
1020 110 115 120
1021 Arg Asp Thr Val Cys Gly Cys Arg Lys Asn Gln Tyr Arg His Tyr
1022 125 *gap?* 130 135
1023 Trp Ser Glu Asn Leu Phe Gln Cys Phe Asn Cys Ser Leu Cys Leu
1024 140 145 150
1025 Asn Gly Thr Val His Leu Ser Cys Gln Glu Lys Gln Asn Thr Val
1026 155 160 165
1027 Cys Thr Cys His Ala Gly Phe Phe Leu Arg Glu Asn Glu Cys Val
1028 170 175 180
1029 Ser Cys Ser Asn Cys Lys Lys Ser Leu Glu Cys Thr Lys Leu Cys
1030 185 190 195
1031 Leu Pro Gln Ile Glu Asn Val Lys Gly Thr Glu Asp Ser Gly Thr
1032 200 205 210
1033 Thr Val Leu Leu Pro Leu Val Ile Phe Phe Gly Leu Cys Leu Leu
1034 215 *gap?* 220 225
1035 Ser Leu Leu Phe Ile Gly Leu Met Tyr Arg Tyr Gln Arg Trp Lys
1036 230 235 240
1037 Ser Lys Leu Tyr Ser Ile Val Cys Gly Lys Ser Thr Pro Glu Lys
1038 245 250 255
1039 Glu Gly Glu Leu Glu Gly Thr Thr Thr Lys Pro Leu Ala Pro Asn
1040 260 265 270
1041 Pro Ser Phe Ser Pro Thr Pro Gly Phe Thr Pro Thr Leu Gly Phe
1042 275 280 285

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INPUT SET: S31123.raw

1043 Ser Pro Val Pro Ser Ser Thr Phe Thr Ser Ser Ser Thr Tyr Thr
1044 290 295 300
1045 Pro Gly Asp Cys Pro Asn Phe Ala Ala Pro Arg Arg Glu Val Ala
1046 305 310 315
1047 Pro Pro Tyr Gln Gly Ala Asp Pro Ile Leu Ala Thr Ala Leu Ala
1048 320 325 330
1049 Ser Asp Pro Ile Pro Asn Pro Leu Gln Lys Trp Glu Asp Ser Ala
1050 335 340 345
1051 His Lys Pro Gln Ser Leu Asp Thr Asp Asp Pro Ala Thr Leu Tyr
1052 350 355 360
1053 Ala Val Val Glu Asn Val Pro Pro Leu Arg Trp
1054 365 370
1055

1056 (2) INFORMATION FOR SEQ ID NO:67:

1057

1058 (i) SEQUENCE CHARACTERISTICS:

--> 1059 (A) LENGTH:6464 bases

1060 (B) TYPE:nucleic acid

1061 (C) STRANDEDNESS:single

1062 (D) TOPOLOGY:linear

1063

1064 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:67:

1065

1066 TCGACATTGA TTATTGACTA GTTATTAATA GTAATCAATT ACGGGGTCAT 50
1067 TAGTTCATAG CCCATATATG GAGTTCGCGG TTACATAACT TACGGTAAAT 100 GGCCCGCCTC GCTGACCGCC C
1068 CTGGCATTAT GCCCAGTACA TGACCTTATG GGACTTTCCT ACTIGGCAGT 350 ACATCTACGT ATTAGTCATC G
1069 AGAACCCACT GCTTAACTGG CTTATCGAAA TTAATACGAC TCACATATAGG 650 GAGACCCAAG CTTCTGCAGG T
1070 AGGTTTTACT TGCTTTAAAA AACCTCCAC ACCTCCCCCT GAACCTGAAA 1250 CATAAAATGA ATGCAATTGT T
1071 GTTAAAAGAT GTATCCTGGA CCTGCCAGAC CTGGCCATTC ACGTAAACAG 1550 AAGATTCCGC CTCAAGTTCC G
1072 CCCACCACCT GGCCCGCCC CGTTGAGGAC AGAAGAAACC CCGGGCAGCC 1850 GCAGCCAAGG CGGACGGGTA G
1073 CGGGCCACGC CGGACTGGGC GGGGCCGGCC TGGTGGAGG GGAGTCTGAC 2150 CTCGTGGAGG CGGGCCTCT G
1074 TGGCTGGATT GGGTTAGGGA AACCGAGGCG GTTCGCTGAA TCGGGTCGAG 2450 CACTTGGCGG AGACGCGCGG G
1075 GAACGAGTTC AAGTACTTCC AAAGAATGAC CACCACCTCC TCAGTGAAG 2750 GTAAACAGAA CCTGGTGATT A
1076 AGGCCATCTC AGACTCTTTG TGACAAGGAT CATGCAGGAA TTTGAAAGTG 3050 ACACGTTCTT CCCAGAAATT G
1077 GCAGAGCTAG AACTCAGACT TTAAAGAAAA TTAGATCAAA GTAGAGACTG 3650 AATTATTCTG CACATCAGAC T
1078 ATGCATCTCA ATTAGTCAGC AACCAGGTGT GGAAAGTCCC CAGGCTCCCC 4000 AGCAGGCAGA AGTATGCAAA G
1079 CTGTAGCGGC GCATTAAGCG CGGCGGGTGT GGTGGTTACG CGCAGCGTGA 4255 CCGCTACACT TGCCAGCGCC C
1080 GTCGCCCTTA TTCCCTTTTT TGCGGCATTT TGCCTTCCTG TTTTGTCTCA 4850 CCCAGAAACG CTGGTGAAAG T
1081 GAAAAGCATC TTACGGATGG CATGACAGTA AGAGKATTAT GCAGTGCTGC 5150 CATAACCATG AGTGATAACA C
1082 TGGATGGAGG CGGATAAAGT TGCAGGACCA CTTCTGCGCT CGGCCCTTCC 5450 GGCTGGCTGG TTTATTGCTG A
1083 AAAAGGATCT AGGTGAAGAT CCTTTTGTAT AATCTCATGA CCAAATCCC 5750 TTAACGTGAG TTTTCGTTCC A
1084 GTAGCACCGC CTACATACCT CGCTCTGCTA ATCCTGTTAC CAGTGGCTGC 6100 TGCCAGTGGC GATAAGTCGT G
1085 GGAAACGCCT GGTATCTTTA TAGTCCTGTC GGGTTTCGCC ACCTCTGACT 6400 TGAGCGTCGA TTTTGTGAT G
1086

1087 (2) INFORMATION FOR SEQ ID NO:68:

1088

1089 (i) SEQUENCE CHARACTERISTICS:

--> 1090 (A) LENGTH:2173 bases

1091 (B) TYPE:nucleic acid

1092 (C) STRANDEDNESS:single

1093 (D) TOPOLOGY:linear

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INPUT SET: S31123.raw

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1094
1095 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:68:
1096
1097 GAATTCCTTT TCTCCGAGTT TTCTGAACTC TGGCTCATGA TCGGGCTTAC 50 TGGATACGAG AATCCTG
1098
--> 1099 ATG GGT CTC CCC ATC GTG CCT GGC CTG CTG CTG TCA CTG GTG CTC 289
1100 Met Gly Leu Pro Ile Val Pro Gly Leu Leu Leu Ser Leu Val Leu
1101 5 10 15
1102
1103 CTG GCT CTG CTG ATG GGG ATA CAC CCA TCA GGG GTC ACC GGA CTG 334
1104 Leu Ala Leu Leu Met Gly Ile His Pro Ser Gly Val Thr Gly Leu
1105 20 25 30
1106
1107 GTT CCT TCT CTT GGT GAC CGG GAG AAG AGG GAT AAT TTG TGT CCC 379
1108 Val Pro Ser Leu Gly Asp Ara Glu Lys Arg Asp Asn Leu Cys Pro
1109 35 40 45
1110
1111 CAG GGA AAG TAT GCC CAT CCA AAG AAT AAT TCC ATC TGC TGC ACC 424
1112 Gln Gly Lys Tyr Ala His Pro Lys Asn Asn Ser Ile Cys Cys Thr
1113 50 55 60
1114
1115 AAG TGC CAC AAA GGA ACC TAC TTG GTG AGT GAC TGT CCA AGC CCA 469
1116 Lys Cys His Lys Gly Thr Tyr Leu Val Ser Asp Cys Pro Ser Pro
1117 65 70 75
1118
1119 GGG CAG GAA ACA GTC TGC GAG CTC TCT CAT AAA GGC ACC TTT ACA 514
1120 Gly Gln Glu Thr Val Cys Glu Leu Ser His Lys Gly Thr Phe Thr
1121 80 85 90
1122
1123 GCT TCG CAG AAC CAC GTC AGA CAG TGT CTC AGT TGC AAG ACA TGT 559
1124 Ala Ser Gln Asn His Val Arg Gln Cys Leu Ser Cys Lys Thr Cys
1125 95 100 105
1126
1127 CGG AAA GAA ATG TTC CAG GTG GAG ATT TCT CCT TGC AAA GCT GAC 604
1128 Arg Lys Glu Yet Phe Gln Val Glu Ile Ser Pro Cys Lys Ala Asp
1129 110 115 120
1130
--> 1131 ATG GAC ACC GTG TGT GGC TGC AAG GAG AAG CAA TTC CAG CGC TAC 649
1132 Met Asp Thr Val Cys Gly Cys Lys Lys Asn Gln Phe Gln Arg Tyr
1133 125 130 135
1134
1135 CTG AGT GAG ACG CAT TTC CAG TGT GTG GAC TGC AGC CCC TGC TTC 694
1136 Leu Ser Glu Thr His Phe Gln Cys Val Asp Cys Ser Pro Cys Phe
1137 140 145 150
1138
1139 AAT GGC ACC GTG ACA ATC CCC TGT AAG GAG AAA CAG AAC ACC GTG 739
1140 Asn Gly Thr Val Thr Ile Pro Cys Lys Glu Lys Gln Asn Thr Val
1141 155 160 165
1142
1143 TGT AAC TGC CAC GCA GGA TTC TTT CTA AGC GGA AAT GAG TGC ACC 784
1144 Cys Asn Cys His Ala Gly Phe Phe Leu Ser Gly Asn Glu Cys Thr
1145 170 175 180
1146

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General review and disproof

use upper-case letters

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--> 1147 CCT TGC AGC CAC TGC AAG AAA AAT CAG GAA TGT ATG AAG CTG TGC 829
 1148 Pro Cys Ser His Cys Lys Lys Asn Gln Glu Cys Met Lys Leu Cys
 1149 185 190 195
 1150
 1151 CTA CCT CCA GTT GCA AAT GTC ACA AAC CCC CAG GAC TCA GGT ACT 874
 1152 Leu Pro Pro Val Ala Asn Val Thr Asn Pro Gln Asp Ser Gly Thr
 1153 200 205 210
 1154 *Generalized for use as the sequence for N^o and explained in (ix) FEATURE section*
 1155 GCC GGC CTG TTG CCT CTG GTT ATC TTC CTA GGT CTT TGC CTT TTA 919
 1156 Ala Val Leu Leu Pro Leu Val Ile Phe Leu Gly Leu Cys Leu Leu
 1157 215 220 225
 1158
 1159 TTC TTT ATC TGC ATC AGT CTA CTG TGC CGA TAT CCC CAG TGG AGG 964
 1160 Phe Phe Ile Cys Ile Ser Leu Leu Cys Arg Tyr Pro Gln Trp Arg
 1161 230 235 240
 1162
 1163 CCC AGG GTC TAC TCC ATC ATT TGT AGG GAT TCA GCT CCT GTC AAA 1009
 1164 Pro Arg Val Tyr Ser Ile Ile Cys Arg Asp Ser Ala Pro Val Lys
 1165 245 250 255
 1166
 1167 GAG GTG GAG GGT GAA GGA ATT GTT ACT AAG CCC CTA ACT CCA GCC 1054
 1168 Glu Val Glu Gly Glu Gly Ile Val Thr Lys Pro Leu Thr Pro Ala
 1169 260 265 270
 1170
 1171 TCT ATC CCA GCC TTC AGC CCC AAC CCC GGC TTC AAC CCC ACT CTG 1099
 1172 Ser Ile Pro Ala Phe Ser Pro Asn Pro Gly Phe Asn Pro Thr Leu
 1173 275 280 285
 1174
 1175 GGC TTC AGC ACC ACC CCA CGC TTC AGT CAT CCT GTC TCC AGT ACC 1144
 1176 Gly Phe Ser Thr Thr Pro Arg Phe Ser His Pro Val Ser Ser Thr
 1177 290 295 300
 1178
 1179 CCC ATC AGC CCC GTC TTC GGT CCT AGT AAC TGG CAC AAC TTC GTG 1189
 1180 Pro Ile Ser Pro Val Phe Gly Pro Ser Asn Trp His Asn Phe Val
 1181 305 310 315
 1182
 1183 CCA CCT GTA AGA GAG GTG GTC CCA ACC CAG GGT GCT GAC CCT CTC 1234
 1184 Pro Pro Val Arg Glu Val Val Pro Thr Gln Gly Ala Asp Pro Leu
 1185 320 325 330
 1186
 1187 CTC TAC GGA TCC CTC AAC CCT GTG CCA ATC CCC GCC CCT GTT CGG 1279
 1188 Leu Tyr Gly Ser Leu Asn Pro Val Pro Ile Pro Ala Pro Val Arg
 1189 335 340 345
 1190
 1191 AAA TGG GAA GAC GTC GTC GCG GCC CAG CCA CAA CGG CTT GAC ACT 1324
 1192 Lys Trp Glu Asp Val Val Ala Ala Gln Pro Gln Arg Leu Asp Thr
 1193 350 355 360
 1194
 1195 GCA GAC CCT GCG ATG CTG TAT GCT GTG GTG GAT GGC GTG CCT CCG 1369
 1196 Ala Asp Pro Ala Met Leu Tyr Ala Val Val Asp Gly Val Pro Pro
 1197 365 370 375
 1198
 1199 ACA CGC TGG AAG GAG TTC ATG CGG CTC CTG GGG CTG AGC GAG CAC 1414

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1200 Thr Arg Trp Lys Glu Phe Met Arg Leu Leu Gly Leu Ser Glu His
1201                               380                               385                               390
1202
1203 GAG ATC GAG CGG TTG GAG CTG CAG AAC GGG CGT TGC CTC CGC GAG 1459
1204 Glu Ile Glu Arc Leu Glu Leu Gln Asn Gly Arg Cys Leu Arg Glu
1205                               395                               400                               405
1206
1207 GCT CAT TAC AGC ATG CTG GAA GCC TGG CGG CGC CGC ACA CCG CGA 1504
1208 Ala His Tyr Ser Met Leu Glu Ala Trp Arg Arg Arg Thr Pro Arg
1209                               410                               415                               420
1210
1211 CAC GAG GCC ACG CTG GAC GTA GTG GGC CGC GTG CTT TGC GAC ATG 1549
1212 His Glu Ala Thr Leu Asp Val Val Gly Arg Val Leu Cys Asp Met
1213                               425                               430                               435
1214
1215 AAC CTG CGT GGC TGC CTG GAG AAC ATC CGC GAG ACT CTA GAA AGC 1594
1216 Asn Leu Arg Gly Cys Leu Glu Asn Ile Arg Glu Thr Leu Glu Ser
1217                               440                               445                               450
1218
1219 CCT GCC CAC TCG TCC ACG ACC CAC CTC CCG CGA TAAGGCCACA 1637
1220 Pro Ala His Ser Ser Thr Thr His Leu Pro Arg
1221                               455                               460
1222
1223 CCCCCACCTC AGGAACGGGA CTCGAAGGAC CATCCTGCTA GATGCCCTGC 1687 TTCCCTGTGA ACCTCCT
--> 1224 GGGAAAGTGTG CCATCTGCTC CCAGACAGCT GAGGGTGCCA AAAGCCAGGA 1887
1225 GAGGTGATTG TGGAGAAAAA GCACAATCTA TCTGATACCC ACTTGGGATG 1937
1226 CAAGGACCCA AACAAAGCTT CTCAGGGCCT CCTCAGTTGA TTTCTGGGCC 1987
1227 CTTTTCACAG TAGATAAAAC AGTCTTTGTA TTGATTATAT CACACTAATG 2037
1228 GATGAACGGT TGAACCTCCCT AAGGTAGGGG CAAGCACAGA ACAGTGGGGT 2087
1229 CTCCAGCTGG AGCCCCCGAC TCTTGTAAT ACATAAAAAA TCTAAAAGTG 2137
1230 AAAAAAAAAA AAAAAAAAAA AAAAAAAAAAG GAATTC 2173
1231

1232 (2) INFORMATION FOR SEQ ID NO:69:
1233
1234 (i) SEQUENCE CHARACTERISTICS:
--> 1235 (A) LENGTH:461 amino acids
--> 1236 (B) TYPE:polypeptide
1237
--> 1238 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:69:
1239
1240 Met Gly Leu Pro Ile Val Pro Gly Leu Leu Leu Ser Leu Val Leu
1241                               5                               10                               15
1242 Leu Ala Leu Leu Met Gly Ile His Pro Ser Gly Val Thr Gly Leu
1243                               20                               25                               30
1244 Val Pro Ser Leu Gly Asp Ara Glu Lys Arg Asp Asn Leu Cys Pro
1245                               35                               40                               45
1246
1247 Gln Gly Lys Tyr Ala His Pro Lys Asn Asn Ser Ile Cys Cvs Thr
1248                               50                               55                               60
1249 Lys Cys His Lys Gly Thr Tyr Leu Val Ser Asp Cys Pro Ser Pro
1250                               65                               70                               75
1251 Gly Gln Glu Thr Val Cys Glu Leu Ser His Lys Gly Thr Phe Thr

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1252					80				85				90		
1253	Ala	Ser	Gln	Asn	His	Val	Arg	Gln	Cys	Leu	Ser	Cys	Lys	Thr	Cys
1254					95					100					105
1255	Arg	Lys	Glu	Yet	Phe	Gln	Val	Glu	Ile	Ser	Pro	Cys	Lys	Ala	Asp
1256					110					115					120
1257	Met	Asp	Thr	Val	Cys	Gly	Cys	Lys	Lys	Asn	Gln	Phe	Gln	Arg	Tyr
1258					125					130					135
1259	Leu	Ser	Glu	Thr	His	Phe	Gln	Cys	Val	Asp	Cys	Ser	Pro	Cys	Phe
1260					140					145					150
1261	Asn	Gly	Thr	Val	Thr	Ile	Pro	Cys	Lys	Glu	Lys	Gln	Asn	Thr	Val
1262					155					160					165
1263	Cys	Asn	Cys	His	Ala	Gly	Phe	Phe	Leu	Ser	Gly	Asn	Glu	Cys	Thr
1264					170					175					180
1265	Pro	Cys	Ser	His	Cys	Lys	Lys	Asn	Gln	Glu	Cys	Met	Lys	Leu	Cys
1266					185					190					195
1267	Leu	Pro	Pro	Val	Ala	Asn	Val	Thr	Asn	Pro	Gln	Asp	Ser	Gly	Thr
1268					200					205					210
1269	Ala	Val	Leu	Leu	Pro	Leu	Val	Ile	Phe	Leu	Gly	Leu	Cys	Leu	Leu
1270					215					220					225
1271	Phe	Phe	Ile	Cys	Ile	Ser	Leu	Leu	Cys	Arg	Tyr	Pro	Gln	Trp	Arg
1272					230					235					240
1273	Pro	Arg	Val	Tyr	Ser	Ile	Ile	Cys	Arg	Asp	Ser	Ala	Pro	Val	Lys
1274					245					250					255
1275	Glu	Val	Glu	Gly	Glu	Gly	Ile	Val	Thr	Lys	Pro	Leu	Thr	Pro	Ala
1276					260					265					270
1277	Ser	Ile	Pro	Ala	Phe	Ser	Pro	Asn	Pro	Gly	Phe	Asn	Pro	Thr	Leu
1278					275					280					285
1279	Gly	Phe	Ser	Thr	Thr	Pro	Arg	Phe	Ser	His	Pro	Val	Ser	Ser	Thr
1280					290					295					300
1281	Pro	Ile	Ser	Pro	Val	Phe	Gly	Pro	Ser	Asn	Trp	His	Asn	Phe	Val
1282					305					310					315
1283	Pro	Pro	Val	Arg	Glu	Val	Val	Pro	Thr	Gln	Gly	Ala	Asp	Pro	Leu
1284					320					325					330
1285	Leu	Tyr	Gly	Ser	Leu	Asn	Pro	Val	Pro	Ile	Pro	Ala	Pro	Val	Arg
1286					335					340					345
1287	Lys	Trp	Glu	Asp	Val	Val	Ala	Ala	Gln	Pro	Gln	Arg	Leu	Asp	Thr
1288					350					355					360
1289	Ala	Asp	Pro	Ala	Met	Leu	Tyr	Ala	Val	Val	Asp	Gly	Val	Pro	Pro
1290					365					370					375
1291	Thr	Arg	Trp	Lys	Glu	Phe	Met	Arg	Leu	Leu	Gly	Leu	Ser	Glu	His
1292					380					385					390
1293	Glu	Ile	Glu	Arc	Leu	Glu	Leu	Gln	Asn	Gly	Arg	Cys	Leu	Arg	Glu
1294					395					400					405
1295	Ala	His	Tyr	Ser	Met	Leu	Glu	Ala	Trp	Arg	Arg	Arg	Thr	Pro	Arg
1296					410					415					420
1297	His	Glu	Ala	Thr	Leu	Asp	Val	Val	Gly	Arg	Val	Leu	Cys	Asp	Met
1298					425					430					435
1299	Asn	Leu	Arg	Gly	Cys	Leu	Glu	Asn	Ile	Arg	Glu	Thr	Leu	Glu	Ser
1300					440					445					450
1301	Pro	Ala	His	Ser	Ser	Thr	Thr	His	Leu	Pro	Arg				
1302					455					460					
1303															

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1413
1414 (i) SEQUENCE CHARACTERISTICS:
--> 1415 (A) LENGTH: 340 amino acids
--> 1416 (B) TYPE: polypeptide
1417
--> 1418 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 71:
1419
1420 Met Gly Leu Ser Thr Val Pro Asp Leu Leu Leu Pro Leu Val Leu
1421                      5                      10                      15
1422 Leu Glu Leu Leu Val Gly Ile Tyr Pro Ser Gly Val Ile Gly Leu
1423                      20                      25                      30
1424 Val Pro His Leu Gly Asp Arg Glu Lys Arg Asp Ser Val Cys Pro
1425                      35                      40                      45
1426
1427 Gln Gly Lys Tyr Ile His Pro Gln Asn Asn Ser Ile Cys Cys Thr
1428                      50                      55                      60
1429 Lys Cys His Lys Gly Thr Tyr Leu Tyr Asn Asp Cys Pro Gly Pro
1430                      65                      70                      75
1431 Gly Gln Asp Thr Asp Cys Arg Glu Cys Glu Ser Gly Ser Phe Thr
1432                      80                      85                      90
1433 Ala Ser Glu Asn His Leu Arg His Cys Leu Ser Cys Ser Lys Cys
1434                      95                      100                     105
1435 Arg Lys Glu Met Gly Gln Val Glu Ile Ser Ser Cys Thr Val Asp
1436                      110                     115                     120
1437 Arg Asp Thr Val Cys Gly Cys Arg Lys Asn Gln Tyr Arg His Tyr
1438                      125                     130                     135
1439 Trp Ser Glu Asn Leu Phe Gln Cys Phe Asn Cys Ser Leu Cys Leu
1440                      140                     145                     150
1441 Asn Gly Thr Val His Leu Ser Cys Gln Glu Lys Gln Asn Thr Val
1442                      155                     160                     165
1443 Cys Thr Cys His Ala Gly Phe Phe Leu Arg Glu Asn Glu Cys Val
1444                      170                     175                     180
1445 Ser Cys Ser Asn Cys Lys Lys Ser Leu Glu Cys Thr Lys Leu Cys
1446                      185                     190                     195
1447 Leu Pro Gln Ile Glu Asn Val Lys Gly Thr Glu Asp Ser Gly Thr
1448                      200                     205                     210
1449 Thr Val Leu Leu Pro Leu Val Ile Phe Phe Gly Leu Cys Leu Leu
1450                      215                     220                     225
1451 Ser Leu Leu Phe Ile Gly Leu Met Tyr Arg Tyr Gln Arg Trp Lys
1452                      230                     235                     240
1453 Ser Lys Leu Tyr Ser Ile Val Cys Gly Lys Ser Thr Pro Glu Lys
1454                      245                     250                     255
1455 Glu Gly Glu Leu Glu Gly Thr Thr Thr Lys Pro Leu Ala Pro Asn
1456                      260                     265                     270
1457 Pro Ser Phe Ser Pro Thr Pro Gly Phe Thr Pro Thr Leu Gly Phe
1458                      275                     280                     285
1459 Ser Pro Val Pro Ser Ser Thr Phe Thr Ser Ser Ser Thr Tyr Thr
1460                      290                     295                     300
1461 Pro Gly Asp Cys Pro Asn Phe Ala Ala Pro Arg Arg Glu Val Ala
1462                      305                     310                     315
1463 Pro Pro Tyr Gln Gly Ala Asp Pro Ile Leu Ala Thr Ala Leu Ala
1464                      320                     325                     330
1465 Ser Asp Pro Ile Pro Asn Pro Leu Gln Lys

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PATENT APPLICATION US/08/383,676DATE: 03/22/1999
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INPUT SET: S31123.raw

1466 335 340
1467
1468

1469 (2) INFORMATION FOR SEQ ID NO:72:
1470
1471 (i) SEQUENCE CHARACTERISTICS:
1472 (A) LENGTH:19 bases
1473 (B) TYPE:nucleic acid
1474 (C) STRANDEDNESS:single
1475 (D) TOPOLOGY:linear
1476
1477 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:72:
1478
1479 GTACTTGAAC TCGTTCCTG
1480
1481
1482
1483
1484
1485
1486
1487

*last sequence in
file*

19

SEQUENCE VERIFICATION REPORT

PATENT APPLICATION US/08/383,676

DATE: 03/22/1999
TIME: 13:50:58

INPUT SET: S31123.raw

Line	Error	Original Text
9	Number of Sequences (64) Doesn't Equal Actual Count (71)	(iii) NUMBER OF SEQUENCES:64
26	Wrong application Serial Number	(A) APPLICATION NUMBER:08/484,312
42	Entered (1365) and Calc. Seq. Length (0) differ	(A) LENGTH:1365 bases
54	Entered (483) and Calc. Seq. Length (0) differ	(A) LENGTH:483 bases
66	Entered (455) and Calc. Seq. Length (0) differ	(A) LENGTH:455 amino acids
67	Wrong or Missing Sequence Type	(B) TYPE:polypeptide
69	Wrong Or Missing Strandedness Value	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:
69	Wrong or Missing Sequence Topology	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:
137	Entered (161) and Calc. Seq. Length (0) differ	(A) LENGTH:161 amino acids
138	Wrong or Missing Sequence Type	(B) TYPE:polypeptide
140	Wrong Or Missing Strandedness Value	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:
140	Wrong or Missing Sequence Topology	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:
168	Entered (157) and Calc. Seq. Length (0) differ	(A) LENGTH:157 bases
180	Entered (13) and Calc. Seq. Length (0) differ	(A) LENGTH:13 amino acids
181	Wrong or Missing Sequence Type	(B) TYPE:polypeptide
183	Wrong Or Missing Strandedness Value	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:
183	Wrong or Missing Sequence Topology	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:
191	Entered (11) and Calc. Seq. Length (0) differ	(A) LENGTH:11 amino acids
192	Wrong or Missing Sequence Type	(B) TYPE:polypeptide
194	Wrong Or Missing Strandedness Value	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:
194	Wrong or Missing Sequence Topology	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:
202	Entered (12) and Calc. Seq. Length (0) differ	(A) LENGTH:12 amino acids
203	Wrong or Missing Sequence Type	(B) TYPE:polypeptide
205	Wrong Or Missing Strandedness Value	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:
205	Wrong or Missing Sequence Topology	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:
213	Entered (13) and Calc. Seq. Length (0) differ	(A) LENGTH:13 amino acids
214	Wrong or Missing Sequence Type	(B) TYPE:polypeptide
216	Wrong Or Missing Strandedness Value	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:
216	Wrong or Missing Sequence Topology	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:
224	Entered (14) and Calc. Seq. Length (0) differ	(A) LENGTH:14 amino acids
225	Wrong or Missing Sequence Type	(B) TYPE:polypeptide
227	Wrong Sequence Number	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:
227	Wrong Or Missing Strandedness Value	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:
227	Wrong or Missing Sequence Topology	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:
232	Sequence * missing	(12) INFORMATION FOR SEQ ID NO:11:
235	Entered (15) and Calc. Seq. Length (0) differ	(A) LENGTH:15 amino acids
236	Wrong or Missing Sequence Type	(B) TYPE:polypeptide
238	Wrong Or Missing Strandedness Value	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:
238	Wrong or Missing Sequence Topology	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:
246	Entered (13) and Calc. Seq. Length (0) differ	(A) LENGTH:13 amino acids
247	Wrong or Missing Sequence Type	(B) TYPE:polypeptide
249	Wrong Or Missing Strandedness Value	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:
249	Wrong or Missing Sequence Topology	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:
257	Entered (13) and Calc. Seq. Length (0) differ	(A) LENGTH:13 amino acids
258	Wrong or Missing Sequence Type	(B) TYPE:polypeptide
260	Wrong Or Missing Strandedness Value	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:
260	Wrong or Missing Sequence Topology	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:
268	Entered (20) and Calc. Seq. Length (0) differ	(A) LENGTH:20 amino acids

SEQUENCE VERIFICATION REPORT

PATENT APPLICATION US/08/383,676

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Line	Error	Original Text
269	Wrong or Missing Sequence Type	(B) TYPE:polypeptide
271	Wrong Or Missing Strandedness Value	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:
271	Wrong or Missing Sequence Topology	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:
281	Entered (19) and Calc. Seq. Length (0) differ	(A) LENGTH:19 amino acids
282	Wrong or Missing Sequence Type	(B) TYPE:polypeptide
284	Wrong Or Missing Strandedness Value	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:
284	Wrong or Missing Sequence Topology	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:
294	Entered (18) and Calc. Seq. Length (0) differ	(A) LENGTH:18 amino acids
295	Wrong or Missing Sequence Type	(B) TYPE:polypeptide
297	Wrong Or Missing Strandedness Value	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:
297	Wrong or Missing Sequence Topology	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:
307	Entered (14) and Calc. Seq. Length (0) differ	(A) LENGTH:14 amino acids
308	Wrong or Missing Sequence Type	(B) TYPE:polypeptide
310	Wrong Or Missing Strandedness Value	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:17:
310	Wrong or Missing Sequence Topology	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:17:
318	Entered (14) and Calc. Seq. Length (0) differ	(A) LENGTH:14 amino acids
319	Wrong or Missing Sequence Type	(B) TYPE:polypeptide
321	Wrong Or Missing Strandedness Value	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:18:
321	Wrong or Missing Sequence Topology	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:18:
329	Entered (13) and Calc. Seq. Length (0) differ	(A) LENGTH:13 amino acids
330	Wrong or Missing Sequence Type	(B) TYPE:polypeptide
332	Wrong Or Missing Strandedness Value	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:19:
332	Wrong or Missing Sequence Topology	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:19:
484	Entered (14) and Calc. Seq. Length (0) differ	(A) LENGTH:14 amino acids
485	Wrong or Missing Sequence Type	(B) TYPE:polypeptide
487	Wrong Or Missing Strandedness Value	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:32:
487	Wrong or Missing Sequence Topology	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:32:
495	Entered (14) and Calc. Seq. Length (0) differ	(A) LENGTH:14 amino acids
496	Wrong or Missing Sequence Type	(B) TYPE:polypeptide
498	Wrong Or Missing Strandedness Value	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:33:
498	Wrong or Missing Sequence Topology	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:33:
650	Entered (51) and Calc. Seq. Length (0) differ	(A) LENGTH:51 amino acids
651	Wrong or Missing Sequence Type	(B) TYPE:polypeptide
653	Wrong Or Missing Strandedness Value	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:46:
653	Wrong or Missing Sequence Topology	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:46:
667	Entered (158) and Calc. Seq. Length (0) differ	(A) LENGTH:158 bases
765	Entered (63) and Calc. Seq. Length (0) differ	(A) LENGTH:63 bases
777	Entered (64) and Calc. Seq. Length (0) differ	(A) LENGTH:64 bases
813	Entered (81) and Calc. Seq. Length (0) differ	(A) LENGTH:81 bases
873	Entered (30) and Calc. Seq. Length (18) differ	(A) LENGTH:30 bases
885	Entered (1334) and Calc. Seq. Length (1134) differ	(A) LENGTH:1334 bases
894	# of Sequences for line conflicts w/ running total	TAGCTGTCTG GC
1000	Entered (371) and Calc. Seq. Length (0) differ	(A) LENGTH:371 amino acids
1001	Wrong or Missing Sequence Type	(B) TYPE:polypeptide
1003	Wrong Or Missing Strandedness Value	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:66:
1003	Wrong or Missing Sequence Topology	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:66:
1059	Entered (6464) and Calc. Seq. Length (50) differ	(A) LENGTH:6464 bases
1090	Entered (2173) and Calc. Seq. Length (1727) differ	(A) LENGTH:2173 bases

SEQUENCE VERIFICATION REPORT
PATENT APPLICATION US/08/383,676DATE: 03/22/1999
TIME: 13:50:59**INPUT SET: S31123.raw**

Line	Error	Original Text
1099	# of Sequences for line conflicts w/ running total	ATG GGT CTC CCC ATC GTG CCT GGC CTG CTG CT
1131	Wrong Nucleic Acid Designator	ATG GAC ACC GTG TGT GGC TGC AAG PAG AkC CA
1131	# of Sequences for line conflicts w/ running total	ATG GAC ACC GTG TGT GGC TGC AAG PAG AkC CA
1155	Wrong Nucleic Acid Designator	GCC GIC CTG TTG CCT CTG GTT ATC TTC CTA GGT
1155	# of Sequences for line conflicts w/ running total	GCC GIC CTG TTG CCT CTG GTT ATC TTC CTA GGT
1224	# of Sequences for line conflicts w/ running total	GGGAAGTGTG CCATCTGCTC CCAGACAGCT GAGGG
1235	Entered (461) and Calc. Seq. Length (0) differ	(A) LENGTH:461 amino acids
1236	Wrong or Missing Sequence Type	(B) TYPE:polypeptide
1238	Wrong Or Missing Strandedness Value	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:69:
1238	Wrong or Missing Sequence Topology	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:69:
1415	Entered (340) and Calc. Seq. Length (0) differ	(A) LENGTH:340 amino acids
1416	Wrong or Missing Sequence Type	(B) TYPE:polypeptide
1418	Wrong Or Missing Strandedness Value	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:71:
1418	Wrong or Missing Sequence Topology	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:71: